SEQUENCE LISTING

<110> Munger, Karl and Syken, Josh	
<120> Methods and Reagents to Regulate Apoptosis	
<130> HMV-054.01 <160> 6 <170> PatentIn version 3.0	
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140 145 150

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Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg 50 55 60

Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr 65 70 75 80

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Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
100 105 110

Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp 115 120 125

Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val 130 135 140

Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala 145 150 155 160

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Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn 225 230 235 240

Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys 245 250 255

Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg 260 265 270

Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro 275 280 285

Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val 290 295 300

Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met 305 310 315 320

Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser 325 330 335

Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile 340 345 350

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,	(2)) SE(() () ()	TION QUENC A) LI B) T C) S	CE CI ENGTI YPE: IRANI	HARACH: 14 nucl DEDNI	CTER: 143 l Leic ESS:	ISTIC pase acic not	CS: pai: d		5						
		(ix)) MOI) FE (1 (1) SE(LECUI ATURI A) NA B) L(QUEN(LE TY E: AME/I OCAT: CE DI	KEY: ION: ESCRI	mRNA CDS 1	A 1440 ON: :	-								
		(ix) (xi) GCT) MO)) FE; (; () SE(GCG	LECUI ATURI A) NA B) L(LE TY E: AME/I CCATY CE DI TGC	YPE: KEY: ION: ESCRI	mRNA CDS 1 IPTIO ACA	A 1440 ON: 5 CGC	TGG	TTG	CTG						48
N	Met 1 CCG	(xi) GCT Ala) MOI) FEZ (1 (1)) SE(GCG Ala CTG	LECUI ATURI A) NI B) LO QUENO CGG	LE TY E: AME/I CCATY CE DI TGC Cys 5 GCT	XEY: ION: ESCRI TCC Ser ATA	CDS 1 IPTIC ACA Thr	1440 DN: S CGC Arg	TGG Trp AGA	TTG Leu 10 GGG	CTG Leu GCC	Val CGG	Val CCG	Val CCC	Gly 15 AGG	Thr GAG	48 96
M C	Met 1 CCG Pro	(ix) (xi) GCT Ala CGG Arg) MOJ) FEZ (1 (1)) SEG GCG Ala CTG Leu	LECUI ATURI A) NA B) LO QUENO CGG Arg CCG Pro	LE TY E: AME/I CCATT CE DI TGC Cys 5 GCT Ala GCA	YPE: XEY: ION: ESCRI TCC Ser ATA Ile	mRNA CDS 1 IPTIC ACA Thr TCG Ser CTG	A 1440 DN: S CGC Arg GGT Gly	TGG Trp AGA Arg 25 CGC	TTG Leu 10 GGG Gly AAG	CTG Leu GCC Ala CTG	Val CGG Arg AGC	Val CCG Pro	Val CCC Pro 30 CCC	Gly 15 AGG Arg	Thr GAG Glu TTT	
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	Met 1 CCG Pro GGC GLY GCG Ala CCT	(ix) (xi) GCT Ala CGG Arg GTG Val TCT Ser 50 GGT	MOD FEX (1) SEG GCG Ala CTG Leu GTG Val 35 TCC Ser	LECUI ATURI A) NA B) LO QUENO CGG Arg CCG Pro 20 GGG Gly CTG Leu	LE TY E: AME/I CE DI TGC Cys 5 GCT Ala GCA Ala ACC Thr	XPE: XEY: ION: ESCRITCC Ser ATA Ile TGG Trp TCT Ser ACA	CDS 1 IPTIO ACA Thr TCG Ser CTG Leu TGC Cys 55 GGA	AGC GGC GLY ACA	TGG Trp AGA Arg 25 CGC Arg CCC Pro	TTG Leu 10 GGG Gly AAG Lys CGA Arg	CTG Leu GCC Ala CTG Leu GCG Ala	CGG Arg AGC Ser CTG Leu 60 CCT	CCG Pro GTC Val 45 CTG Leu	CCC Pro 30 CCC Pro ACA Thr	Gly 15 AGG Arg GCC Ala TTG Leu	Thr GAG Glu TTT Phe AGA Arg	96
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	Met 1 1 200 200 200 200 200 200 200 200 200	(ix) (xi) GCT Ala CGG Arg GTG Val TCT Ser 50 GGT Gly TCC Ser	MOD FEX (1) SEG GCG Ala CTG Leu GTG Val 35 TCC Ser GTC Val TTC Phe	LECUI ATURI A) NA B) LO QUENO CGG Arg CCG Pro 20 GGG Gly CTG Leu AGC Ser CAC His	LE TY E: AME/I CE DI TGC Cys 5 GCT Ala Ala ACC Thr Leu ACG Thr 85 CCT	XPE: XEY: ION: ESCRITCC Ser ATA Ile TGG Trp TCT Ser ACA Thr 70 AGT Ser CGA	CDS 1 IPTIO ACA Thr TCG Ser CTG Leu TGC Cys 55 GGA Gly GCC Ala AAT	AGC GGC GGC ACA Thr CCT Pro	TGG Trp AGA Arg 25 CGC Arg CCC Pro AAA Lys TTG Leu AGC	TTG Leu 10 GGG Gly AAG Lys CGA Arg CAT His GCC Ala 90 CAG	CTG Leu GCC Ala CTG Leu GCG Ala AAC Asn 75 AAA Lys	CGG Arg AGC Ser CTG Leu 60 CCT Pro GAA Glu	CCG Pro GTC Val 45 CTG Leu TTC Phe GAT Asp	CCC Pro 30 CCC Pro ACA Thr ATT Ile TAT Tyr	Gly 15 AGG Arg GCC Ala TTG Leu TGT Cys TAT Tyr 95 AAA	Thr GAG Glu TTT Phe AGA Arg ACT Thr 80 CAG	96 144 192 240

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																132
Pro	цуs 130	Ala	ьуѕ	GIU	гуз	135	ser	GIII	ьеи	Ala	140	Ala	TÀT	GIU	Val	
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145	2011	1106	-	· 0.1	150		-10	0_11	-1-	155		-1-	1		160	
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aaa	aaa	maa	aaa		777	7 00	200	777		aaa	COTT	thichida Thichida	CTC		COT	816
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	116	FIU	vaı	FLO		Gry	Val	Giu	дор	-	0.111	T 11 T	vai	H. 9		
305	~-~				310					315		~~~	~~~		320	
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ma c	030		7 (17)	770	ama	3 00		aaa	COM	aaa	7 (717)		א מיא	C A C	CAG	1152
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															Leu	
- 1	1			405				_1 2	410	3			_1.5	415		
∆ממ	≱מר	רכב	ርልር		AGC	CTC	ልጥሮ	רידים		ጥልሮ	מרת	מאמ	CAC		ACA	1296
			Crit	CAU		-19		-10		+110		CAU	Cric	CAU	* 7017	1270

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1443

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val

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Glu 465	Asp	Glu	Glu	Gly	Phe 470	Leu	Ser	Lys	Leu	Lys 475	Lys	Met	Phe	Thr	Ser 480	
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	(xi) SE	QUENC	CE DI	ESCR:	IPTI	ON:	SEQ :	ID N	0:3:						
Met	GCT Ala			Cys					Leu					Gly		4.8
1 CCG	CGG	כידכ	CCG	5 යථආ	מיזי מ	ייר <i>י</i> כ	CCT	אמא	10	acc	ccc	CCG	מממ	15	GNG	96
	Arg															,
GGC	GTG	GTG	GGG	GCA	TGG	CTG	AGC	CGC	AAG	CTG	AGC	GTC	CCC	GCC	TTT	144
Gly	Val	Val 35	Gly	Ala	Trp	Leu	Ser 40	Arg	Lys	Leu	Ser	Val 45	Pro	Ala	Phe	
	TCT															192
	Ser 50					55	_		•		60					
	GGT Gly															240
	TCC Ser									AAA					CAG Gln	288
ልሞል																
	TTA Leu			CCT										AAA Lys	GCC	336

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						Phe										
	130		*		-	135					140		•			
TTG	AGT	GAT	GAG	GTG	AAG	AGG	AAG	CAG	TAC	GAT	GCC	TAC	GGC	TCT	GCA	480
						Arg										
145		•			150	_	-		_	155		•	-		160	
GGC	TTC	GAT	CCT	GGG	GCC	AGC	GGC	TCC	CAG	CAT	AGC	TAC	TGG	AAG	GGA	528
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly	
_		-		165					170					175		
GGC	CCC	ACT	GTG	GAC	CCC	GAG	GAG	CTG	TTC	AGG	AAG	ATC	TTT	GGC	GAG	576
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu	
			180					185					190			
TTC	TCA	TCC	TCT	TCA	TTT	GGA	GAT	TTC	CAG	ACC	GTG	TTT	GAT	CAG	CCT	624
Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro	
		195					200					205				
						TTG										672
Gln		Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln		Ala	Lys	Gly	Val	
	210					215					220					
						AAC										720
	Lys	Glu	Phe	Thr		Asn	Ile	Met	Asp		Cys	Glu	Arg	Cys		
225					230					235					240	
						GGC										768
GIY	гàг	GIY	Asn		Pro	Gly	Thr	ьуs		GIn	His	Cys	Hls		Cys	
000	aaa	maa	000	245	O 7 7	7.00	3 mg	220	250	222	COE	mmm	ama	255	aam	01.0
						ACC										816
GIY	GTÀ	ser		Met	GIU	Thr	тте		THE	GTÀ	PLO	ые		Met	Arg	
TOO	א מכ	ייניטיט	260	አርሜ	יייטיי	GGT	aaa	265	acc	Trece	እጥሮ	አጥሮ	270 גיזיג	TOCA	CCC	864
						Gly										004
501	1111	275	1119	9	Oy D	O ₁	280	2129	Q±y	501	+10	285		201	110	
TGT	GTG		TGC	AGG	GGA	GCA		CAA	GCC	AAG	CAG		AAG	CGA	GTG	912
						Ala										
-1-	290		-1	5	1	295	2			-1 -	300	-2-	-1-	3		
ATG	ATC	CCT	GTG	CCT	GCA	GGA	GTC	GAG	GAT	GGC	CAG	ACC	GTG	AGG	ATG	960
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met	
305					310	-			_	315					320	
CCT	GTG	GGA	AAA	AGG	GAA	ATT	TTC	ATT	ACG	TTC	AGG	GTG	CAG	AAA	AGC	1008
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser	
				325					330					335		
CCT	GTG	TTC	CGG	AGG	GAC	GGC	GCA	GAC	ATC	CAC	TCC	GAC	CTC	TTT	ATT	1056
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile	
			340					345					350			
						CTT										1104
Ser	Ile		Gln	Ala	Leu	Leu	_	Gly	Thr	Ala	Arg		Gln	Gly	Leu	
	~-~	355				- ~~	360	~~~	~~~	~~~	3 OF	365	2 62	~~~	G 2 G	1150
						ACG										1152
Tyr		Thr	TTE	ASI	vaı	Thr	TTE	Pro	Pro	GIY		GIN	unr	Asp	GIN	
ממ	370	aaa	» ma	ааш	aaa	375	aaa	70 TH C1	aaa	aaa	380	777	700	ma c	aaa	1200
						AAA										1200
ьуs 385	TT6	Arg	MEC	GTĀ	390	Lys	ату	116	FLO	395	176	usil	PGT	TÄŢ	400	
	GGA	GZC	ሮልሮ	ТΔС		ሮልሮ	Δጥሮ	ልልር	ልጥል		Chu	CCA	ልልር	AGG	CTA	1248
						His										1440
~ I ~	7	יייי	A. J. N.	405			~	-10	410	3			-15	415		
ACG	AGC	CGG	CAG			CTG	ATC	CTG		TAC	GCC	GAG	GAC		ACA	1296
							_		_			_		_		

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Thr Ser Arq Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr 420 425 GAT GTG GAG GGG ACG GTG AAC GGC GTC ACC CTC ACC AGC TCT GGA AAA 1344 Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Lys 440 435 AGA TCC ACT GGA AAC TAG 1362 Arg Ser Thr Gly Asn 450

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr 5 10 Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu 25 Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg 55 Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr 70 Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln 85 90 Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala 105 Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp 120 Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val 135 140 Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala 150 155 Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly 165 170 Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu 180 185 Phe Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro 200 Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val 215 220 Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn 230 235 Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys 245 250 Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg 265 Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro 280 Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val 295 300 Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met 310

Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser

315

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325 330 Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile 345 Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu 360 Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln 375 Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly 390 395 400 Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu 405 410 415 Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr 420 425 Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Lys 440 Arg Ser Thr Gly Asn 450